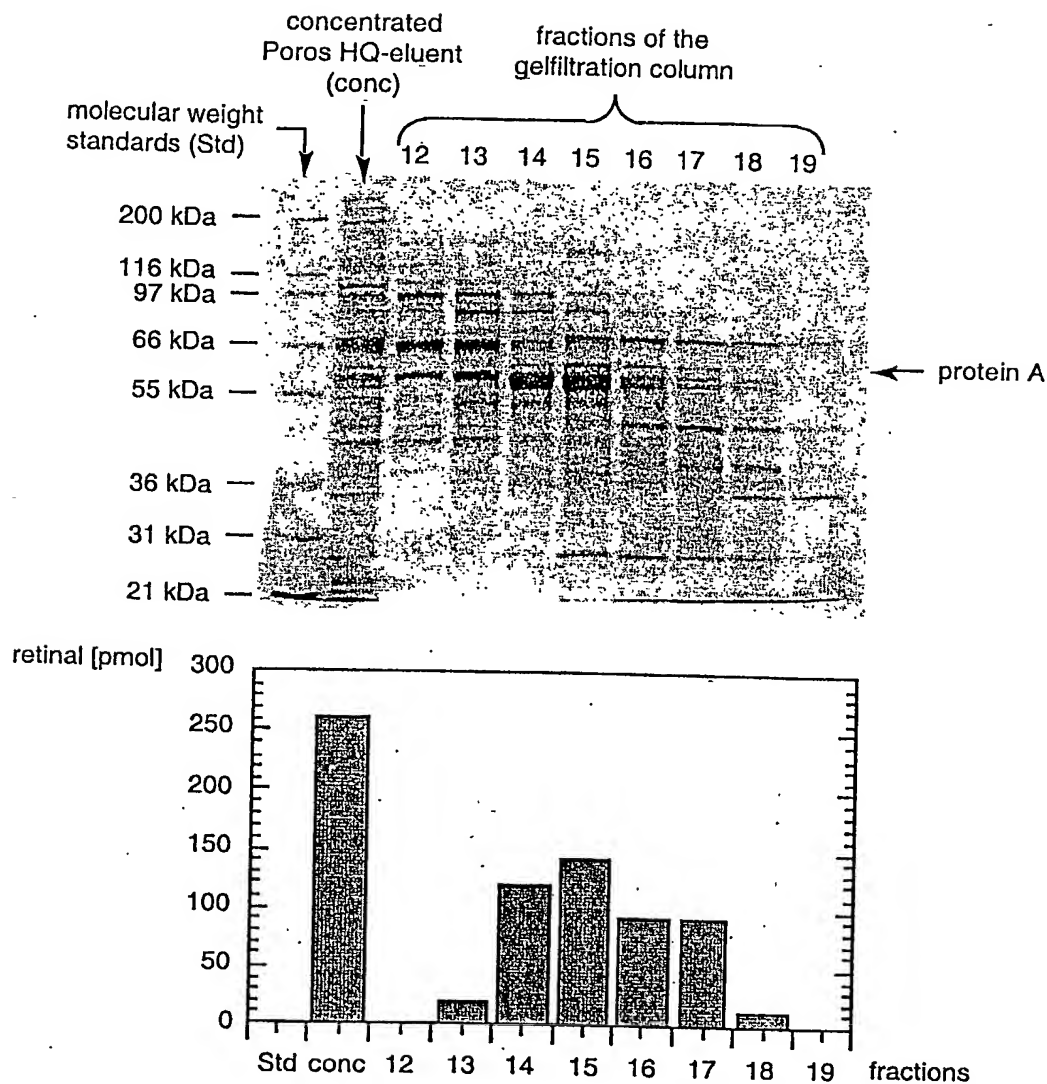




11/11/2002 10:00:00

Figure 1



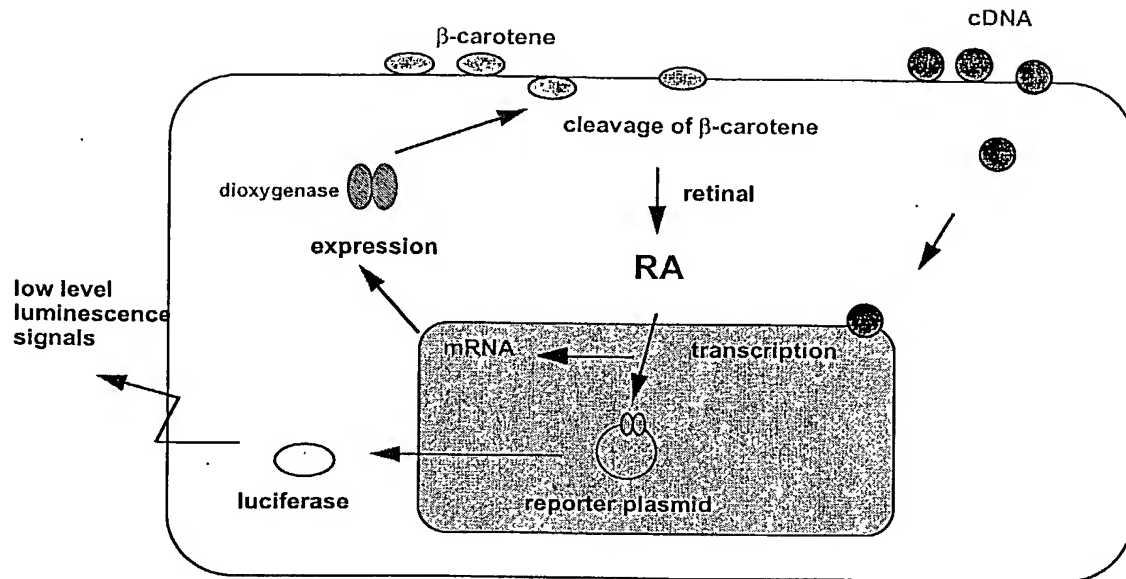


Figure 2



10057197 100503

Figure 3
No. 2

Seq. ID

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101 AGGAGCAGCT GGGTAGAGGA CACAGGAGAG CGATGGAGAC
AATATTTAAC

151 AGAAACAAAG AAGAGCATCC AGAGCCCATA AAAGCTGAGG
TGCAAGGTCA

201 GTTGCCCACT TGGTTGCAAG GGGTACTTCT CCGAAATGGC
CCAGGGATGC

251 ACACAATAGG GGACACTAAA TACAACCACT GGTTTGATGG
CTTGGCTCTG

301 CTGCACAGCT TCACGTTTAA AAATGGTGAA GTTACTACA
GAAGTAAGTA

351 CCTCCGAAGT GACACATACA ACTGCAATAT AGAAGCAAAC
CGAATCGTGG

401 TGTCTGAGTT TGAACCATG GCTTATCCGG ATCCATGCAA
AAACATATTT

451 GCCAAGGCAT TCTCATACTT ATCTCACACC ATTCTGAGT
TCACGGACAA

501 CTGCCTGATC AACATTATGA AAAGTGGGGA TGATTATTAT
GCTACCAAGT

551 AGACTAACTT CATCAGAAAA ATTGATCCAC AGACTCTGGA
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601 AAGGTAGACT ACAGCAAATA TGTAAGCTGTA AACTTGGCAA
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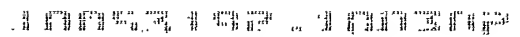
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701 ATAAAGGGAG AACAAAATAT GTTCTCTTTA AGATCCCTTC
CTCTGTACCA

751 GAAAAAGAAA AGAAGAAATC TTGTTTTTAA CACCTGGAAG
TAGTATGCTC

801 CATCCCTTCT CGCTCCCTGC TCAACCAAG CTACTACCAC
AGCTTTGGAA

851 TCACAGAAAA TTATATTGTG TTCATAGAGC AGCCATTTAA
ACTGGATATT



1851 TTTAAGGCAC AGCGATGAGT TTTACTACAG GTAACGATAT
GCACAACCTGG



1 111111 1 1111 1 1111 1111

Figure 4
No. 1

Seq. ID

1 METIFNRNKE EHPEPIKAEV QGQLPTWLQG VLLRNGPGMH
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51 FDGLALLHSF TFKNGEVYR SKYLRSDTYN CNIEANRIVV
SEFGTMAYPD

101 PCKNIFAKAF SYLSHTIPEF TDNCLINIMK TGDDYYATSE
TNFIRKIDPQ

151 TLETLDKVDY SKYVAVNLAT SHPHYDSAGN ILNMGTSIVD
KGRTKYVLFK

201 IPSSVPEKEK KKSCFKHLEV VCSIPSRLL QPSYYHSFGI
TENYIVFIEQ

251 PFKLDIVKLA TAYIRGVNWA SCLSFHKEDK TWFHFVDRKT
KKEVSTKFYT

301 DALVLYHHIN AYEEDGHVVF DIVAYRDNSL YDMFYLLKLD
KDFEVNNKLT

351 SIPTCKRFVV PLQYDKDAEV GSNLVKLPTS ATAVKEKDGS
IYCQPEILCE

401 GIELPRVNYD YNGKKYKYVY ATEVQWSPVP TKIAKLVQOT
KEVLHWGEDH

451 CWPSEPIFVP SPDAREEDEG VVLTCVVVSE PNKAPFLIL
DAKTFKELGR

501 ATVNVEMHLD LHGMFIPQND LGAETE



11/07/2007 14:07:30

Figure 5

Seq ID No. 4 and Seq ID No. 5

57 10 EEHPEPIKA[·]EVQQLPTWLQGVLLR[·]..NGPGMHTIGDTKY[·]NHWF[·]DGLALL[·]
69 20 || | : | | | : | | | | | | : | : | : | | | | |
EELSSPLTAHV[·]TGRIPLWLTGSL[·]LR[·]CFTG[·]PGLFEV[·]GSEPFY[·]HLFDGQALL[·]
105 58 HSFTFKNGEV[·]YYRSKYLRSDTYNCNIEANRIVVSEFG[·]..TMAYPD[·]PC[·]KN[·]I
119 70 | | | | | | : : | | | | | | : | : | | | | | | | | | | |
HKFDFKEGHV[·]TYHRRFIR[·]TDAYVRAMTEKRIVITEFGFTTCAFPD[·]PC[·]KN[·]I
155 106 FAKAFSYLSHTIPEFTDNCLINIMKTGDDY[·]YATSETNFIRKIDPQTLET[·]L
167 120 | : | | | | | : | : | : | : | | | | | | : | : | : | : | : | : | :
FSRFFSYFRGV[·]..EVDNALVNVPVGEDYYACTETNFITKINPETLET[·]I
203 156 ..DKVDYSKY[·]VAVNLATSHPHYDSAGNILNMGT[·]SIVDKGR[·]TKYVLFKIPS[·]
217 168 . | | | | | | | | | | : . | : | . | : | | | | | : | | | |
FTKQVDLCNY[·]SVNGATAHPHIENDGT[·]VYNIGNCFGKNFSIAYNIVKIPP[·]
253 204 SVPEKEKKKSCFKHLEVVC[·]SIPSRSLLOPSYYHSFGITENYIVFIEQPF[·]K
266 218 : | | | | | | : | : | | | | | : | | | | | : | | | | | | | | | |
LQADKEDPISK[·]FTS.EIVVQFPCSDRFKPSYVHSFGLTPNYIVFVETPVK[·]
300 254 LDIVKLATAY[·].IRGVNWASCL.SPHKEDK.TWFHFVDRKTKKEVSTKFYT[·]
316 267 : : | : : : | : | | | | | | | : | : | | | | | : | : | : | : | : | :
INLFKFLSSWSLWGANYMDCFESFTNETMGVWLHIADKKRKKYLNNKYRT[·]
344 301 DALVLYHHINAYEEDGHVVDIVAYRDN[·]SL...YDMFY[·]LKKLDKDFE...
366 317 | : | | | | | : | : | : | : : | : | | | | | | | | | | | | | | | | | | |
SPFNLFHHINTYEDNGFLIVDLCCWKGFEFVYNYFTLYLANLRENWEEVK[·]
391 345 VNNKLTSIPTCKRFVVPLQYDKDAEVGSNLVKLP.TSATAV[·]..KEKDGSI[·]
415 367 | : | : | : | | | | : | | | | | | | | : | : | : | : | : | : | : | : |
KNARKAPQPEVRRYVLPLNIDK.ADTGKNLVTLPNTTATAILCSDEFTTI[·]
436 392 YCQPEILCEG....IELPRVNYD.YNGKKYKYVYATEVQWSPVPTKIAKL[·]
464 416 : : | : | | | : | | | | | | | | | | | | | | : : | : | : | : | : | : | : |
WLEPEVLFSGPRQAFEPQINYQKYCGKPYTYAYGLGLNHF.VPDRLCKL[·]



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437 NVQTKVELH..WGEDHCWPSEPIFVPSPDAREEDEGVVLTCTVVVSEPNKA
484  ||.|||  ||  :|||||||  |||  |||:||||.  ||  .
465 NVKTKETWFTVWQEPDSYPSEPIFVSHPDALIEDDGVVLSVVVSPGAGQK
514
485 P.FLLILDAKTFKELGRA..TVNVEMHLDLHGMF 515
    | :||||.||  |.  ||  ||  :  .  .  ||:|
515 PAYLLILNAKDLSEVARAEFTVEINIPVTFHGLF 548

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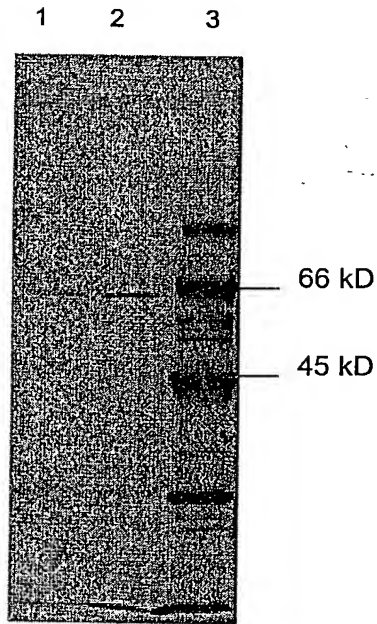


Fig. 6



1.0057197 1.0003012

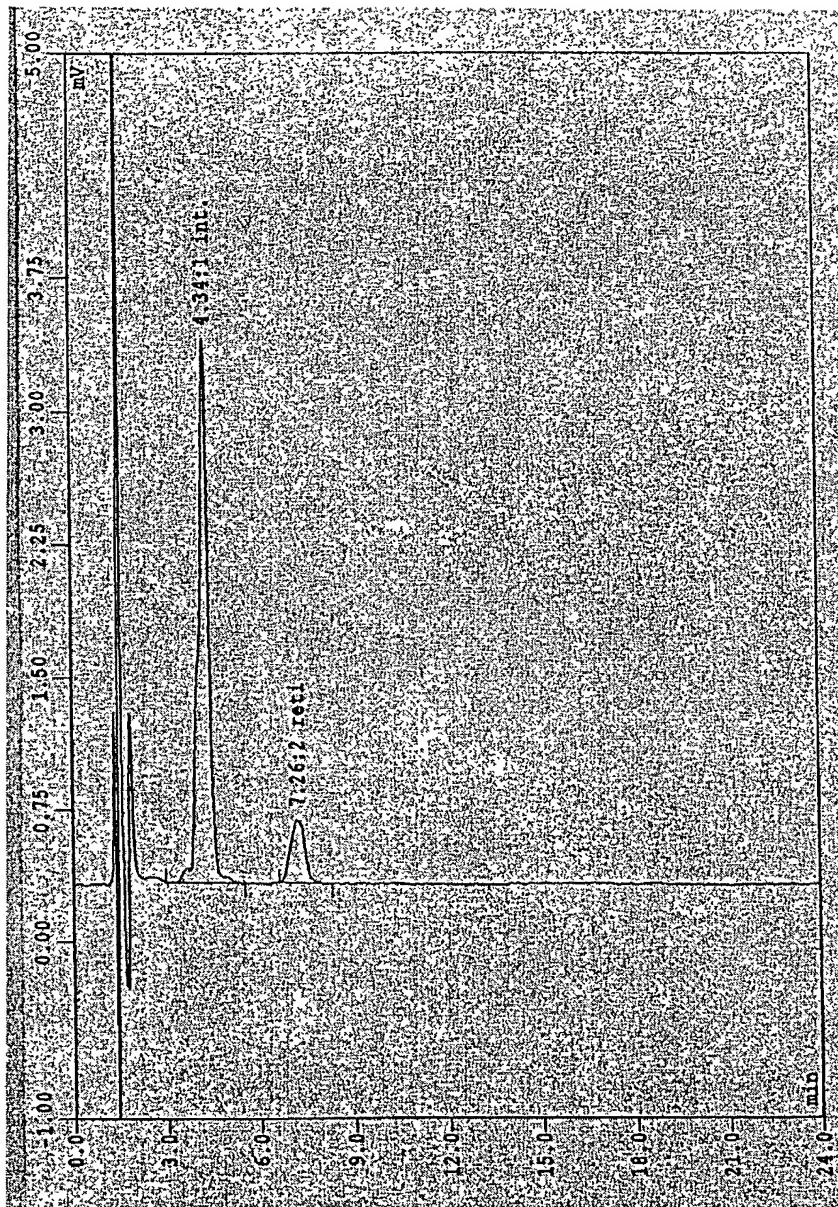


Fig. 7



10053192 100302

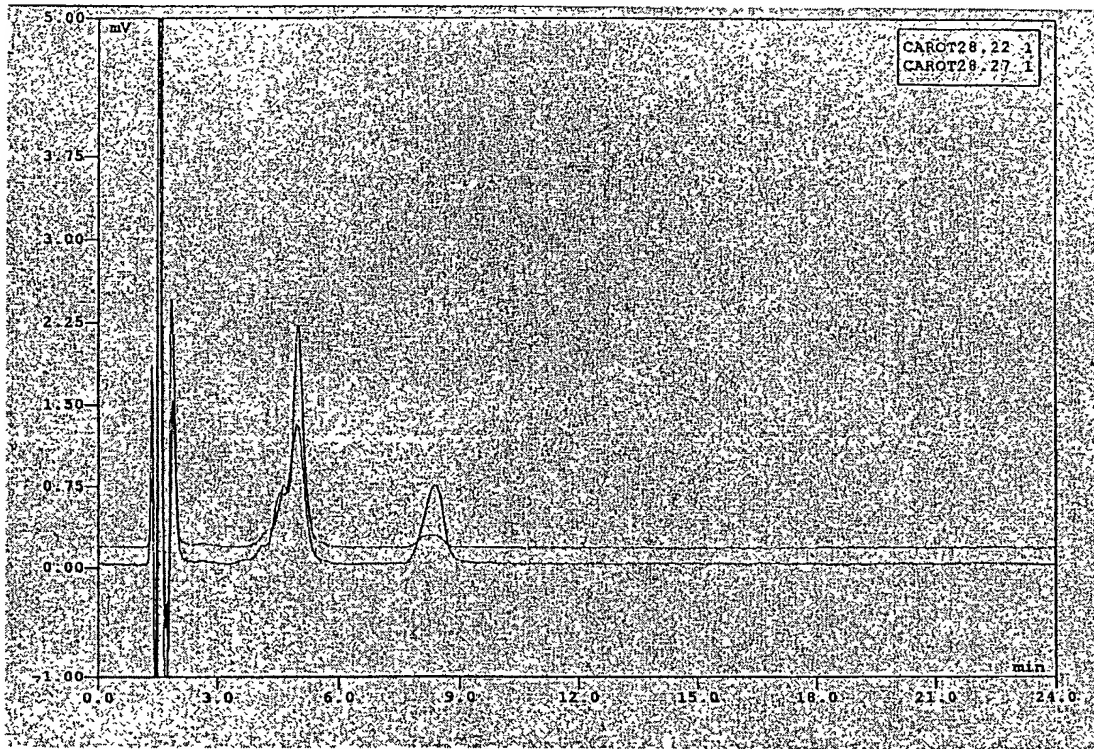


Fig. 8